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nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; and then

- 5 (c) amplifying the nucleic acid [present in the sample] template via the PCR using the plurality of first PCR primers and the plurality of second PCR primers; whereby a subset of the plurality first primers binds to the consensus sequence of interest substantially wherever it occurs in the [sample] template, and a subset of the plurality of second primers binds to the [sample] template at locations removed from the first primers such that DNA regions flanked by the first primer and the second primer are [specifically] amplified.

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2. (AMENDED) The method of Claim 1, wherein the [sample containing nucleic acid contains] template is genomic DNA.
3. (AMENDED) The method of Claim 1, wherein the [sample containing nucleic acid contains] template is eukaryotic genomic DNA.
4. (AMENDED) The method of Claim 1, wherein [the sample containing nucleic acid contains] template is human genomic DNA.
5. (AMENDED) The method of Claim 1, wherein the [sample containing nucleic acid contains] template is prokaryotic DNA.
6. (AMENDED) The method of Claim 1, wherein the [sample containing nucleic acid contains] template is DNA selected from the group consisting of cloned genomic DNA, a subgenomic region of DNA, a chromosome, and a subchromosomal region.
7. (AMENDED) The method of Claim 1, wherein the [sample containing nucleic acid contains] template is RNA.

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12. (AMENDED) A method of [specifically] amplifying exons from a [sample of] DNA template comprising:
- (a) providing a plurality of first PCR primers, each first primer having a region of fixed nucleotide sequence identical or complementary to a consensus sequence of a 3' splice region and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence;
  - (b) providing a plurality of second PCR primers, each second primer having a region of fixed nucleotide sequence reversely complementary to a consensus sequence of a 5' splice region and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; and then
  - (c) amplifying the [genomic] DNA template via the PCR using the plurality of first PCR primers and the plurality of second PCR primers; whereby a subset of the plurality first primers binds to a sequence reversely complementary to the 3' splice consensus sequence substantially wherever it occurs in the [sample] template, and a subset of the plurality of second primers binds to the 5' splice consensus sequence substantially wherever it occurs in the [sample] template, such that exons flanked by the first primer and the second primer are [specifically] amplified [from the sample].
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16. (AMENDED) The method of Claim 12, wherein a genomic DNA template is [specifically] amplified.
17. (AMENDED) The method of Claim 12, wherein a human genomic DNA template is [specifically] amplified.
18. (AMENDED) The method of Claim 12, wherein a DNA template selected from the group consisting of cloned genomic DNA, a subgenomic region of DNA, a chromosome, and a subchromosomal region is [used as the sample DNA] amplified.
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19. (AMENDED) A method of [specifically] amplifying regions flanking a consensus sequence in a [sample of] nucleic acid template of totally or partially unknown sequence comprising:

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- (a) providing a plurality of first PCR primers, each first primer having a region of fixed nucleotide sequence identical or complementary to a consensus sequence of interest and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence;
  - (b) providing a plurality of second PCR primers, each second primer having a region of arbitrary, yet fixed nucleotide sequence and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; then
  - (c) amplifying the nucleic acid [present in the sample] template via the PCR using the plurality of first PCR primers and the plurality of second PCR primers; whereby a subset of the plurality first primers binds to the consensus sequence of interest substantially wherever it occurs in the [sample] template, and a subset of the plurality of second primers binds to the [sample] template at locations removed from the first primers such that DNA regions flanked by the first primer and the second primer are [specifically] amplified; then
  - (d) incorporating the amplified nucleic acid of step (c) into a library;
  - (e) sequencing a portion of amplified nucleic acid from a particular clone from the library of step (d) and providing a third PCR primer of unique sequence which will prime PCR amplification from the sequenced portion of DNA;
  - (f) providing a plurality of fourth PCR primers, each fourth primer having a region of arbitrary, yet fixed nucleotide sequence and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; and then
  - (g) amplifying the nucleic acid present in the [sample] template via the PCR using the third PCR primer and the plurality of fourth PCR primers; whereby the third primer binds to the sequenced portion of nucleic acid from step (e), and a subset of the plurality of fourth primers binds to the [sample] template at

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~~locations removed from the third primers such that DNA regions flanked by the third primer and the fourth primer are [specifically] amplified.~~

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CONC'D*
20. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is genomic DNA.
  21. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is eukaryotic genomic DNA.
  22. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is human genomic DNA.
  23. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is prokaryotic DNA.
  24. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is DNA selected from the group consisting of cloned genomic DNA, a subgenomic region of DNA, a chromosome, and a subchromosomal region.
  25. (AMENDED) The method of Claim 19, wherein the [sample containing nucleic acid contains] template is RNA.

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#### SUPPORT FOR THE AMENDMENT

The word "template" as presented in the amended claims is explicitly defined in the specification at page 19, lines 22-27. The word template is also used throughout the specification. See, for example, page 5, line 27; page 9, lines 23-24; page 11, line 3; page 15, line 10, etc. No new matter is added.